REMARKS

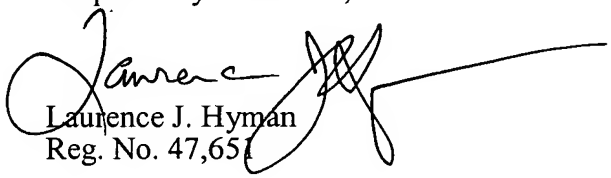
Claims 1-50 are pending in this application. Claims 23 and 29 have been amended by the current amendment. The amendments to claims 23 and 29 insert sequence identifiers in adherence with 37 C.F.R. §§1.821 to 1.825.

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-23, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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Reg. No. 47,651

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San Francisco, California 94111-3834
Tel: 415-576-0200
Fax: 415-576-0300
Attachments
LJH:dmw
60102023 v1

SEQUENCE LISTING

<110> Sherman, Irwin
Winograd, Enrique
The Regents of the University of California

<120> Peptides Which Generate Antibodies Resulting in Lysis of Pathologically Adherent Erythrocytes

<130> 023070-140500US

<140> US 10/663,215
<141> 2003-09-15

<160> 23

<170> PatentIn Ver. 2.1

<210> 1
<211> 911
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<400> 1

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Glu Pro Ala Ala His Asp Thr Glu Ala Thr Ala Thr Asp Tyr His Thr
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Thr Ser His Pro Gly Thr His Glu Val Tyr Val Glu Leu Gln Glu Leu
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Val Met Asp Glu Lys Asn Gln Glu Leu Arg Trp Met Glu Ala Ala Arg
 65                  70                  75                  80

Trp Val Gln Leu Glu Glu Asn Leu Gly Glu Asn Gly Ala Trp Gly Arg
                 85                  90                  95

Pro His Leu Ser His Leu Thr Phe Trp Ser Leu Leu Glu Leu Arg Arg
            100                 105                 110

Val Phe Thr Lys Gly Thr Val Leu Leu Asp Leu Gln Glu Thr Ser Leu
        115                 120                 125

Ala Gly Val Ala Asn Gln Leu Leu Asp Arg Phe Ile Phe Glu Asp Gln
    130                 135                 140

Ile Arg Pro Gln Asp Arg Glu Glu Leu Leu Arg Ala Leu Leu Leu Lys
145                 150                 155                 160

His Ser His Ala Gly Glu Leu Glu Ala Leu Gly Gly Val Lys Pro Ala
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Val Leu Thr Arg Ser Gly Asp Pro Ser Gln Pro Leu Leu Pro Gln His
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Ser Ser Leu Glu Thr Gln Leu Phe Cys Glu Gln Gly Asp Gly Gly Thr
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Glu Gly His Ser Pro Ser Gly Ile Leu Glu Lys Ile Pro Pro Asp Ser
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Glu Ala Thr Leu Val Leu Val Gly Arg Ala Asp Phe Leu Glu Gln Pro
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Val Leu Gly Phe Val Arg Leu Gln Glu Ala Ala Glu Leu Glu Ala Val
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Glu Leu Pro Val Pro Ile Arg Phe Leu Phe Val Leu Leu Gly Pro Glu
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Ala Pro His Ile Asp Tyr Thr Gln Leu Gly Arg Ala Ala Ala Thr Leu
        275                 280                 285

Met Ser Glu Arg Val Phe Arg Ile Asp Ala Tyr Met Ala Gln Ser Arg
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Gly Glu Leu Leu His Ser Leu Glu Gly Phe Leu Asp Cys Ser Leu Val
305                 310                 315                 320

Leu Pro Pro Thr Asp Ala Pro Ser Glu Gln Ala Leu Leu Ser Leu Val
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Pro Val Gln Arg Glu Leu Leu Arg Arg Arg Tyr Gln Ser Ser Pro Ala
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Lys Pro Asp Ser Ser Phe Tyr Lys Gly Leu Asp Leu Asn Gly Gly Pro
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Asp Asp Pro Leu Gln Gln Thr Gly Gln Leu Phe Gly Gly Leu Val Arg
    370                 375                 380

Asp Ile Arg Arg Arg Tyr Pro Tyr Tyr Leu Ser Asp Ile Thr Asp Ala
385                 390                 395                 400

Phe Ser Pro Gln Val Leu Ala Ala Val Ile Phe Ile Tyr Phe Ala Ala
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Leu Ser Pro Ala Ile Thr Phe Gly Gly Leu Leu Gly Glu Lys Thr Arg
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Asn Gln Met Gly Val Ser Glu Leu Leu Ile Ser Thr Ala Val Gln Gly
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Ile Leu Phe Ala Leu Leu Gly Ala Gln Pro Leu Leu Val Val Gly Phe
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Ser Gly Pro Leu Leu Val Phe Glu Glu Ala Phe Phe Ser Phe Cys Glu
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Thr Asn Gly Leu Glu Tyr Ile Val Gly Arg Val Trp Ile Gly Phe Trp
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Ser Leu Ile Phe Ile Tyr Glu Thr Phe Ser Lys Leu Ile Lys Ile Phe
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Gln Asp His Pro Leu Gln Lys Thr Tyr Asn Tyr Asn Val Leu Met Val
545                 550                 555                 560

Pro Lys Pro Gln Gly Pro Leu Pro Asn Thr Ala Leu Leu Ser Leu Val
                565                 570                 575

Leu Met Ala Gly Thr Phe Phe Phe Ala Met Met Leu Arg Lys Phe Lys
            580                 585                 590

Asn Ser Ser Tyr Phe Pro Gly Lys Leu Arg Arg Val Ile Gly Asp Phe
        595                 600                 605

Gly Val Pro Ile Ser Ile Leu Ile Met Val Leu Val Asp Phe Phe Ile
    610                 615                 620

Gln Asp Thr Tyr Thr Gln Lys Leu Ser Val Pro Asp Gly Phe Lys Val
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Ser Asn Ser Ser Ala Arg Gly Trp Val Ile His Pro Leu Gly Leu Arg
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Ser Glu Phe Pro Ile Trp Met Met Phe Ala Ser Ala Leu Pro Ala Leu
            660                 665                 670

Leu Val Phe Ile Leu Ile Phe Leu Glu Ser Gln Ile Thr Thr Leu Ile
        675                 680                 685

Val Ser Lys Pro Glu Arg Lys Met Val Lys Gly Ser Gly Phe His Leu
    690                 695                 700

Asp Leu Leu Leu Val Val Gly Met Gly Gly Val Ala Ala Leu Phe Gly
705                 710                 715                 720

Met Pro Trp Leu Ser Ala Thr Thr Val Arg Ser Val Thr His Ala Asn
                725                 730                 735

Ala Leu Thr Val Met Gly Lys Ala Ser Thr Pro Gly Ala Ala Ala Gln
            740                 745                 750

Ile Gln Glu Val Lys Glu Gln Arg Ile Ser Gly Leu Leu Val Ala Val
        755                 760                 765

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Leu Ala Val Leu Phe Gly Ile Phe Leu Tyr Met Gly Val Thr Ser Leu
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Ser Gly Ile Gln Leu Phe Asp Arg Ile Leu Leu Leu Phe Lys Pro Pro
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Lys Tyr His Pro Asp Val Pro Tyr Val Lys Arg Val Lys Thr Trp Arg
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Met His Leu Phe Thr Gly Ile Gln Ile Ile Cys Leu Ala Val Leu Trp
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Val Val Lys Ser Thr Pro Ala Ser Leu Ala Leu Pro Phe Val Leu Ile
850 855 860

Leu Thr Val Pro Leu Arg Arg Val Leu Leu Pro Leu Ile Phe Arg Asn
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536-545 of AE1 protein, predicted alpha-helix

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<210> 4
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<213> Artificial Sequence

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when used as antigen raises antibodies which bind
to and cause destruction of pathologically
adherent erythrocytes

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1 5 10

<210> 5
<211> 14
<212> PRT
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<220>
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native AE1 sequence, peptide including two
residues on either side of predicted alpha-helix

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<210> 6
<211> 14
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<220>
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<220>
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<223> Xaa = amino acid charged under physiological conditions

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<210> 7
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<210> 8
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<212> PRT
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<220>
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<400> 8
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<210> 9
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<220>
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<212> PRT
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<400> 13
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<212> PRT
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<210> 20
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ID NO:5 or 6

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1 5

<210> 23
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fragment containing amino terminal portion of SEQ
ID NO:5 or 6

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